

Figure 1

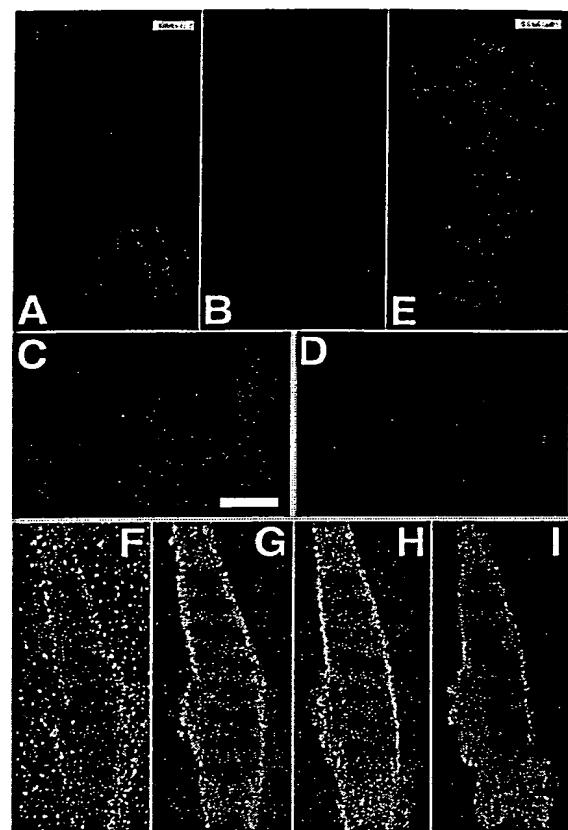


Figure 2

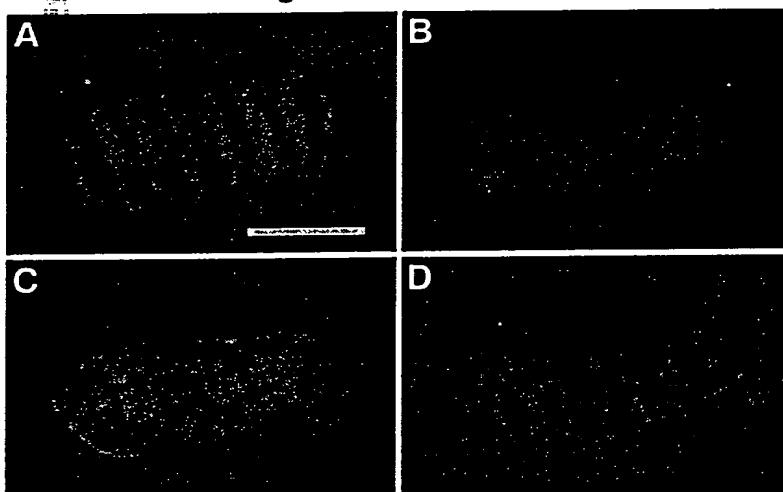


Figure 3

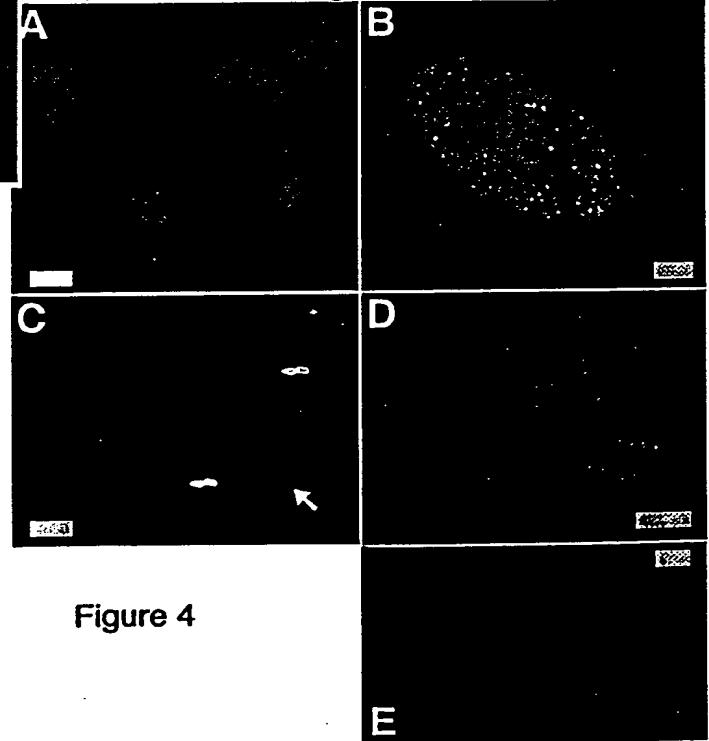


Figure 4



B

EWGRKN-CAIILENDOSISRNHAVLT-ANFSV p95
HSIGRSSSKNPLIKNDKSIISRQHITPKWEINNS xrs2

THEISQRDEIPVTPTKONSHYGTTFVNE-ERMQNG p95
SDIUKHSS-----CLVNRKGRLTSLNKKFMKVGET xrs2

ESRTIHKSCGCTFCFEG---SKFRIEYE p95
-----LNASDVKSTIIELGTEPIRIEPE xrs2

C

	1	2	3	4	5	6	7	8	9
23.9	+	-	-	-	-	-	-	-	-
9.4	-	-	-	-	-	-	-	-	-
6.7	+	-	-	-	-	-	-	-	-
4.4	+	-	-	-	-	-	-	-	-

FIGURE 6

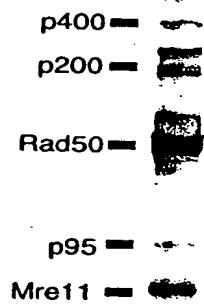


FIGURE 5

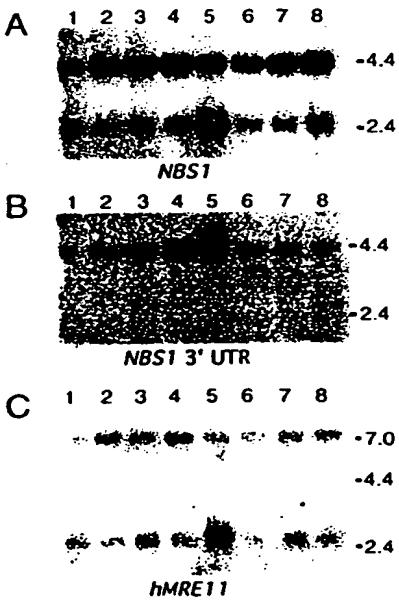


FIGURE 7

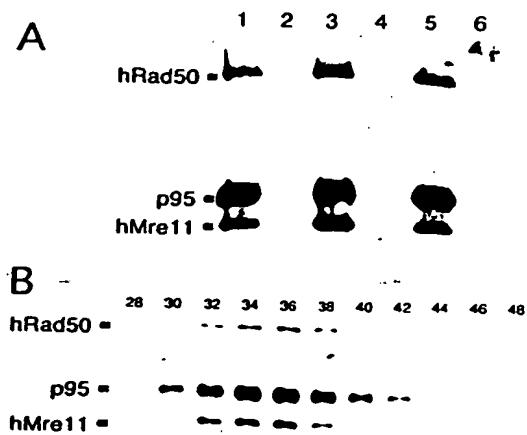


FIGURE 8

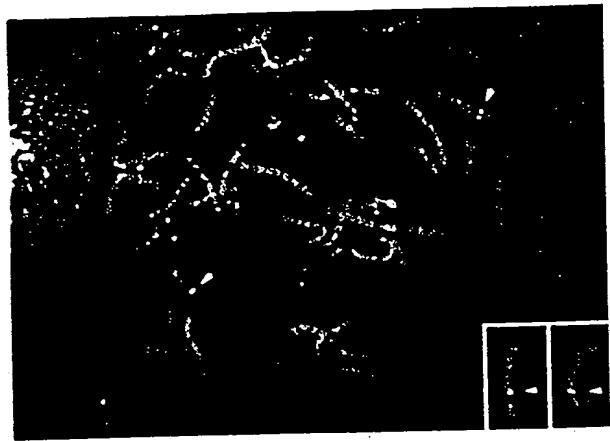


FIGURE 9

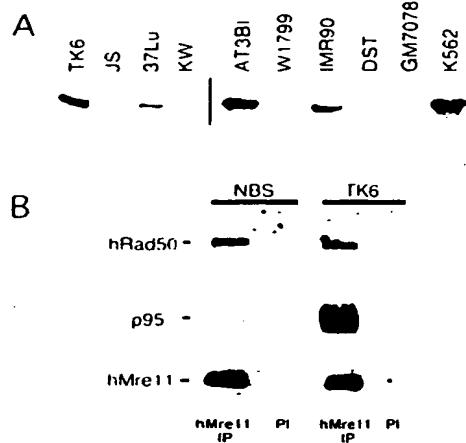


FIGURE 10

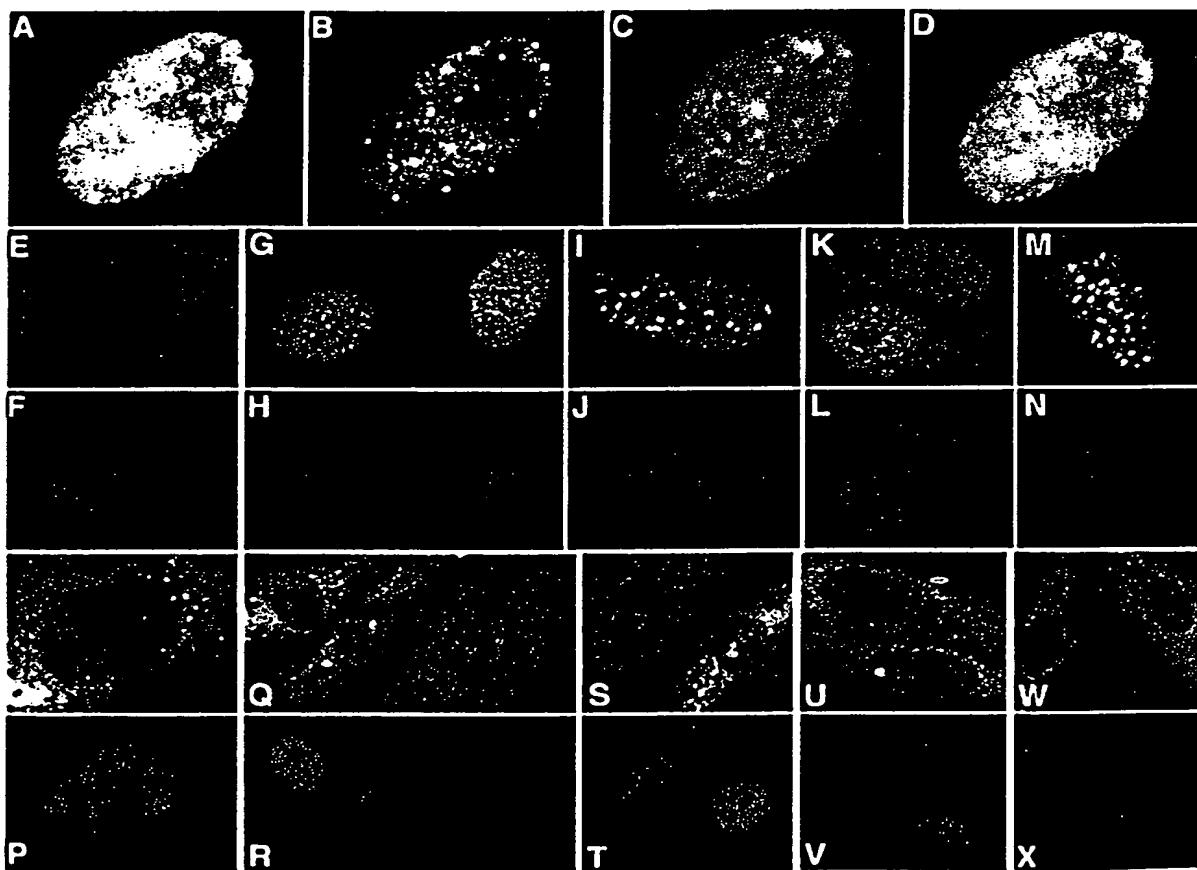


FIGURE 11

Figure 12

Amino Acid	Codon
Phe	UUU, UUC
Ser	UCU, UCC, UCA, UCG, AGU, AGC
Tyr	UAU, UAC
Cys	UGU, UGC
Leu	UUA, UUG, CUU, CUC, CUA, CUG
Trp	UGG
Pro	CCU, CCC, CCA, CCG
His	CAU, CAC
Arg	CGU, CGC, CGA, CGG, AGA, AGG
Gln	CAA, CAG
Ile	AUU, AUC, AUA
Thr	ACU, ACC, ACA, ACG
Asn	AAU, AAC
Lys	AAA, AAG
Met	AUG
Val	GUU, GUC, GUA, GUG
Ala	GCU, GCC, GCA, GCG
Asp	GAU, GAC
Gly	GGU, GGC, GGA, GGG
Glu	GAA, GAG

FIGURE 13

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro	pro
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala	leu
Pro (P)	gly	gly
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

9
8
7
6
5
4
3
2
1

ttcggcacgaggcgcggttgcacgtcgccccagccctgaggagccgaccatgtggaaactgtgcccgcggcc
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gttgcatt
att
gtctccattt
actggccctactatagcatt
aaatatt
ttaatt
atacgtatt
gacaaggtaaaatt
tattatataaacttt
tt
caatt
gct

FIGURE 14

100 200 300 400 500 600 700 800 900

MWKLLPAAGPAGGEPYRLLTGVEYVVGRKNCAILIELDQSISRNHAVLTANFSVTNLSQTDEIPVLTLDNSKYGTFVNE
EKMONGFSRTLKGDGITFGVFGSKFRIEYEPLVACSSCLDVSGKTALNQAILQLGGFTVNNWTEECTHLVMVSVKVTIK
TICALICGRPIVKPEYFTEFLKAVQSKKOPPQIESFYPPLEPSIGSKNVDLSGRQERKQIFKGKTFIFLNAKQHKKLSS
AVVFGGGEARLITEENEEEHNFLAPGTCVVDTGITNSQTLIPDCQKKWIQSIMDMILQRQGLRPIPEAEIGLAVIFMTTK
NYCDPQGHGSTGLKTTPGPSLSQGVSVDEKLMP SAPVNNTTYVADTESEQADTWDLSERPKEIKVSKMEQKFRMLSQDA
PTVKESCKTSSNNNSMVSNTLAKMRIPNYQLSPTKLP SINKSKDRASQQQQTNSIRNYFQPSTKKRERDEENQEMSSCKS
ARIETSCSLLEQTQPATPSLWKQNKEQHLSENEVPDNTSDNNLFDTDLKSIVKNSASKSHAAEKLRSNKKREMDDVAIED
EVLEQLFKDTKPELEIDVVKVQKQEEDVNRKRPRMDIETNDTFSDEAVPESSKISQENEIGKKRELKEDSLWSAKEISNN
DKLQDDSEMLPKKLLTEFRSLVIKNSTS RNP SGINDDYGQLKNFKFKVTVYPGAGKLPHIIGGSDLIAHHARKNTELE
EWLRQEMEVQNQHAKEESSLADDLFRYNPYLKRRR.

FIGURE 15